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Form PTOP1449 US Department of Commerce Patent and Trademark Office AUG 08 2001 PATENT & TRADEMARK OFFICE	ATTY DOCKET NO: P-IS 4584	SERIAL NO. 09/835,072
	APPLICANT: Goodlett and Keller	
INFORMATION DISCLOSURE STATEMENT BY APPLICANT	FILING DATE: April 13, 2001	GROUP: 1651

U.S. PATENT DOCUMENTS

EXAM. INITIALS		DOCUMENT NUMBER	DATE	NAME	CLASS	SUB- CLASS	FILING DATE

FOREIGN PATENT DOCUMENTS

EXAM. INITIALS		DOCUMENT NUMBER	DATE	COUNTRY	CLASS	SUB- CLASS	TRANSLATION (YES/NO)
CGM		EP0387646 A1	12/30/98	Europe	—	—	
↓		WO93/24834	12/9/93	PCT	—	—	

OTHER DOCUMENTS (Including Author, Title, Date, Pertinent Pages)

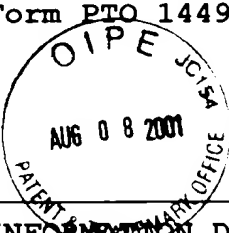
CGM		Berndt et al., "Reliable automatic protein identification from matrix-assisted laser desorption/ionization mass spectrometric peptide fingerprints," <u>Electrophoresis</u> , 20:3521-3526 (1999).
↓		Chen et al., "A dynamic programming approach to de novo peptide sequencing via tandem mass spectrometry," <u>Proceedings of the Eleventh Annual ACM-SIAM Symposium on Discrete Algorithms</u> , San Francisco 389-398 (2000).

EXAMINER <i>C. M. / f</i>	DATE CONSIDERED <i>October 11, 2002</i>
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EXAMINER: Initial if citation considered, whether or not citation is in conformance with MPEP 609; Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.

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CAM		Dančik et al., "De novo peptide sequencing via tandem mass spectrometry," <u>J. Comp. Biol.</u> , 6:327-342 (1999).
		Goodlett et al., "Protein identification with a single accurate mass of a cysteine-containing peptide and constrained database searching," <u>Anal. Chem.</u> , 72:1112-1118 (2000).
		Gygi et al., "Quantitative analysis of complex protein mixtures using isotope-coded affinity tags," <u>Nature Biotechnology</u> , 17:994-999 (1999).
		Horn et al., "Automated de novo sequencing of proteins by tandem high-resolution mass spectrometry," <u>Proc. Natl. Acad. Sci. USA</u> , 97:10313-10317 (2000).
		Keough et al., "A method for high-sensitivity peptide sequencing using postsource decay matrix-assisted laser desorption ionization mass spectrometry," <u>Proc. Natl. Acad. Sci. USA</u> , 96:7131-7136 (1999).
		Nicola et al., "Automation of data collection for matrix-assisted laser desorption/ionization mass spectrometry using a correlative analysis algorithm," <u>Anal. Chem.</u> , 71:3213-3219 (1998).
		Pevzner et al., "Efficiency of database search for identification of mutated and modified proteins via mass spectrometry," <u>Genome Research</u> , 11:290-299 (2001).
		Pevzner et al., "Mutation-tolerant protein identification by mass spectrometry," <u>J. Comp. Biol.</u> , 7(6):777-787 (2000).
✓		Sechi and Chait, "A method to define the carboxyl terminal of proteins," <u>Anal. Chem.</u> , 72:3374-3378 (2000).

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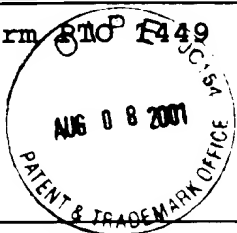
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Form PTO P 449 	US Department of Commerce Patent and Trademark Office	ATTY DOCKET NO: P-IS 4584	SERIAL NO. 09/835,072
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INFORMATION DISCLOSURE STATEMENT BY APPLICANT		FILING DATE: April 13, 2001	GROUP: 1651

CSM		Sechi and Chait, "Modification of cysteine residues by alkylation. A tool in peptide mapping and protein identification," <u>Anal. Chem.</u> , 70:5150-5158 (1998).
↓		Wilm et al., "De novo sequencing of proteins with mass spectrometry using the differential scanning technique," <u>Proteome and Protein Analysis</u> , (Springer) 65-79 (2000).

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